

-240
CAGGAGGTGAAAGTCCCCGGCGGTCCGGATGGCGCAGTTGCACTGCGCTGCTGAGCTCGC -180
GGCCGCCTGCGCACACTGGGGGGACTCGCTTCGGCTAGTAACTCCTCCACCTCGCGGCGG -120
ACGACCGGTCTTGACACGCTGCCTGCGAGGCAAGTTGAACAGTGCAGAGAAGGATCTTA -60
AAGCTACACCCGACTTGCCACGATTGCCTTCAATCTGAAGAACCAGGCTGTTGGAGAG 0

ATGGCAGTGACATCCCACCACATGATCCCGGTGATGGTTGTCCTGATGAGCGCCTGCCTG 60
MetAlaValThrSerHisHisMetIleProValMetValValLeuMetSerAlaCysLeu 20

GCCACCGCCGGTCCAGAGCCCAGCACCCGGTGTGAACTGTCACCAATCAACGCCTCTCAC 120
AlaThrAlaGlyProGluProSerThrArgCysGluLeuSerProIleAsnAlaSerHis 40
↑ & #
CCAGTCCAGGCCCTTGATGGAGAGCTTACCGTTCTGTCTGGCTGTGCCAGCAGAGGCACC 180
ProValGlnAlaLeuMetGluSerPheThrValLeuSerGlyCysAlaSerArgGlyThr 60
+ &
ACCGGGCTGCCAAGGGAGGTCCATGTCCTAAACCTCCGAAGTACAGATCAGGGACCAGGC 240
ThrGlyLeuProArgGluValHisValLeuAsnLeuArgSerThrAspGlnGlyProGly 80

CAGCGGCAGAGAGAGGTTACCCTGCACCTGAACCCATTGCCTCGGTGCACACTCACCAC 300
GlnArgGlnArgGluValThrLeuHisLeuAsnProIleAlaSerValHisThrHisHis 100

AAACCTATCGTGTTCCTGCTCAACTCCCCCAGCCCCTGGTGTGGCATCTGAAGACGGAG 360
LysProIleValPheLeuLeuAsnSerProGlnProLeuValTrpHisLeuLysThrGlu 120

AGACTGGCCGCTGGTGTCCCCAGACTCTTCCTGGTTTTCGGAGGGTTCTGTGGTCCAGTTT 420
ArgLeuAlaAlaGlyValProArgLeuPheLeuValSerGluGlySerValValGlnPhe 140

CCATCAGGAACTTCTCCTTGACAGCAGAAACAGAGGAAAGGAATTTCCCTCAAGAAAAT 480
ProSerGlyAsnPheSerLeuThrAlaGluThrGluGluArgAsnPheProGlnGluAsn 160
+ #
GAACATCTCGTGCCTGGGCCCAAAAGGAATATGGAGCAGTGAAGTTCGTTCACTGAAGTC 540
GluHisLeuValArgTrpAlaGlnLysGluTyrGlyAlaValThrSerPheThrGluLeu 180

AAGATAGCAAGAAACATCTATATTAAAGTGGGAGAAGATCAAGTGTTCCTCCTACGTGT 600
LysIleAlaArgAsnIleTyrIleLysValGlyGluAspGlnValPheProProThrCys 200
&
AACATAGGGAAGAATTTCTCTCACTCAATTACCTTGCCGAGTACCTTCAACCCAAAGCC 660
AsnIleGlyLysAsnPheLeuSerLeuAsnTyrLeuAlaGluTyrLeuGlnProLysAla 220

GCCGAAGGTTGTGTCTGCCCCAGTCAGCCCCATGAAAAGGAAGTACACATCATCGAGTTA 720
AlaGluGlyCysValLeuProSerGlnProHisGluLysGluValHisIleIleGluLeu 240
&
ATTACCCCCAGCTCGAACCCTTACAGCGCTTTCAGGTGGATATAATAGTTGACATACGA 780
IleThrProSerSerAsnProTyrSerAlaPheGlnValAspIleIleValAspIleArg 260

CCTGCTCAAGAGGATCCCGAGGTGGTCAAAAACCTTGTCTGATCTTGAAGTGCAAAAAG 840
ProAlaGlnGluAspProGluValValLysAsnLeuValLeuIleLeuLysCysLysLys 280
&
TCTGTCAACTGGGTGATCAAGTCTTTTGACGTCAAGGGAACTTGAAAGTCATTGCTCCC 900
SerValAsnTrpValIleLysSerPheAspValLysGlyAsnLeuLysValIleAlaPro 300

AACAGTATCGGCTTTGGAAAAGAGAGTGAACGATCCATGACAATGACCAAATTGGTAAGA 960
AsnSerIleGlyPheGlyLysGluSerGluArgSerMetThrMetThrLysLeuValArg 320

GATGACATCCCTTCCACCCAAGAGAATCTGATGAAGTGGGCACTGGACAATGGCTACAGG 1020
AspAspIleProSerThrGlnGluAsnLeuMetLysTrpAlaLeuAspAsnGlyTyrArg 340

FIGURE 1A

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CCAGTGACGTCATACACAATGGCTCCCGTGGCTAATAGATTTTCATCTTCGGCTTGAGAAC	1080
ProValThrSerTyrThrMetAlaProValAlaAsnArgPheHisLeuArgLeuGluAsn	360
AACGAGGAGATGAGAGATGAGGAAGTCCACACCATTCTCCTGAGCTTCGTATCCTGCTG	1140
AsnGluGluMetArgAspGluGluValHisThrIleProProGluLeuArg <u>IleLeuLeu</u>	380
GACCCTGACCACCCGCCCGCCCTGGACAACCCACTCTTCCCAGGAGAGGGAAGCCCAAT	1200
<u>AspProAspHisProProAlaLeu</u> AspAsnProLeuPheProGlyGluGlySerProAsn	400
peptide 1	
GGTGGTCTCCCCTTTCCATTCCCGGATATCCCCAGGAGAGGCTGGAAGGAGGGCGAAGAT	1260
GlyGlyLeuProPheProPheProAspIleProArgArgGlyTrpLysGluGlyGluAsp	420
AGGATCCCCCGGCCAAAGCAGCCCATCGTTCCAGTGTTCAACTGCTTCCTGACCACCGA	1320
ArgIleProArgProLys <u>GlnProIleValProSerValGln</u> LeuLeuProAspHisArg	440
peptide 2	
GAACCAGAAGAAGTGCAAGGGGGCGTGGACATCGCCCTGTCAGTCAAATGTGACCATGAA	1380
GluProGluGluValGlnGlyGlyValAspIleAlaLeuSerValLysCysAspHisGlu	460
&	
AAGATGGTCGTGGCTGTAGACAAAGACTCTTTCCAGACCAATGGCTACTCAGGGATGGAG	1440
LysMetValValAlaValAspLysAspSerPheGlnThrAsnGlyTyrSerGlyMetGlu	480
+	
CTCACCTGTTGGATCCTTCGTGTAAAGCCAAATGAATGGTACTCACTTTGTTCTCGAG	1500
LeuThrLeuLeuAspProSerCysLysAlaLysMetAsnGlyThrHisPheValLeuGlu	500
& #	
TCTCCCCTGAATGGCTGTGGTACTCGACATCGGAGGTGACCCCGGATGGTGTGGTTTAC	1560
SerProLeuAsnGlyCysGlyThrArgHisArgArgSerThrProAspGlyValValTyr	520
&	
TATACTCTATTGTGGTGCAGGCTCCGTCCCCTGGGGATAGCAGTGGCTGGCCTGATGGC	1620
TyrAsnSerIleValValGlnAlaProSerProGlyAspSerSerGlyTrpProAspGly	540
+++	
TATGAAGACTTGGAGTCAGGCGATAATGGATTTCTTGGAGACGGGGATGAAGGAGAACT	1680
TyrGluAspLeuGluSerGlyAspAsnGlyPheProGlyAspGlyAspGluGlyGluThr	560
GCCCCCTGAGCCGAGCTGGAGTGGTGGTGTTTAACTGCAGCTTGCGGCAGCTGAGGAAT	1740
AlaProLeuSerArgAlaGlyValValValPheAsnCysSerLeuArgGlnLeuArgAsn	580
# &	
CCCAGTGGCTTCCAGGGCCAGCTCGATGGAATGCTACCTTCAACATGGAGCTGTATAAC	1800
ProSerGlyPheGlnGlyGlnLeuAspGlyAsnAlaThrPheAsnMetGluLeuTyrAsn	600
#	
ACAGACCTCTTTCTGGTGCCCTCCCCAGGGGTCTTCTCTGTGGCAGAGAACGAGCATGTT	1860
ThrAspLeuPheLeuValProSerProGlyValPheSerValAlaGluAsnGluHisVal	620
TATGTTGAGGTGTCTGTACCAAGGCTGACCAAGATCTGGGATTGCGCCATCCAAACCTGC	1920
TyrValGluValSerValThrLysAlaAspGlnAspLeuGlyPheAlaIleGlnThrCys	640
&	
TTTCTCTCTCCATACTCCAACCCAGACAGAATGTCTGATTACACCATCATCGAGAACATC	1980
PheLeuSerProTyrSerAsnProAspArgMetSerAspTyrThrIleIleGluAsnIle	660
TGTCCGAAAGACGACTCTGTGAAGTTCTACAGCTCCAAGAGAGTGCACTTTCCCATCCCG	2040
CysProLysAspAspSerValLysPheTyrSerSerLysArgValHisPheProIlePro	680
&	
CATGCTGAGGTGGACAAGAAGCGCTTCAGCTTCCTGTTCAAGTCTGTGTTCAACACCTCC	2100
HisAlaGluValAspLysLysArgPheSerPheLeuPheLysSerValPheAsnThrSer	700
#	
CTGCTCTTCTGCACTGCGAGTTGACTCTGTGCTCCAGGAAGAAGGGCTCCCTGAAGCTG	2160
LeuLeuPheLeuHisCysGluLeuThrLeuCysSerArgLysLysGlySerLeuLysLeu	720
& &	

FIGURE 1B

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CCGAGGTGTGTGACTCCTGACGACGCCTGCACCTTCTCTCGATGCCACCATGATCTGGACC	2220
ProArgCysValThrProAspAspAlaCysThrSerLeuAspAlaThrMetIleTrpThr	740
& &	
ATGATGCAGAATAAGAAGACATTACCAAGCCCCTGGCTGTGGTCCTCCAGGTAGACTAT	2280
MetMetGlnAsnLysLysThrPheThrLysProLeuAlaValValLeuGlnValAspTyr	760
AAAGAAAATGTTCCCAGCACTAAGGATTCCAGTCCAATTCTCTCTCCTCCACAGATT	2340
LysGluAsnValProSerThrLysAspSerSerProIleProProProProGlnIle	780
TTCCATGGCCTGGACACGCTCACCGTGATGGGCATTGCATTTGCAGCATTTGTGATCGGA	2400
PheHisGlyLeuAspThrLeuThrValMetGlyIleAlaPheAlaAlaPheValIleGly	800
GCGCTCCTGACGGGGGCCTTGTGGTACATCTACTCCCACACAGGGGAGACAGCACGAAGG	2460
AlaLeuLeuThrGlyAlaLeuTrpTyrIleTyrSerHisThrGlyGluThrAlaArgArg	840
\$ @	
CAGCAAGTCCCTACCTCGCCGCCAGCCTCGGAGAACAGCAGCGCGCCACAGCATCGGC	2520
GlnGlnValProThrSerProProAlaSerGluAsnSerSerAlaAlaHisSerIleGly	860
AGCACTCAGAGTACCCCCTGCTCTAGCAGCAGCACAGCCTAGGTGGACAGACAGACGCC	2580
SerThrGlnSerThrProCysSerSerSerSerThrAla	873
GCCCACCGCAGCCAGGGCAGGGCCCCGATGCCAGTGCTGCGTGTCCACAGTCAGAAGTCTT	2640
GATCTGGGCTCCCTGTAAAGAAAGAGTGAATTTTCAGTATACAGACAGCCAGTTCTACCCA	2700
CCCCTTACCACGGCCCCACATAAATGTGACCCTGGGCATCTGTACACGAAAGCTAAGCTG	2760
GTGGCCTTCCCCACCGCCCTCGCAGGATGGGGGTTTCAATGTGAAACATCTGCCAGTT	2820
TTGTTTTGTTTTTTAATGCTGCTTTGTCCAGGTGTCCAAACATCCATCATTTGGGGTGG	2880
TCTGTTTTTACAGAGTAAAGGAGGCGGTGAAGGGACGTCAGCTAGTGTGTAGAGCCAAGGG	2940
GAGACAGCTAGGATTCTCGCCTAGCTGAACCAAGGTGTAAAATAGAAGACACGCTCC	2997

FIGURE 1C

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>DL;3FF

Meld of: 3FF6-9 3FF13

TTCCGTTGCT GTCGGTTGGC GAGGAGTTTC CTGTTTCCCC CGCAGCGCTG
AGTTGAAGTT GAGTGAGTCA CTCGCGCGCA CGGAGCGACG ACACCCCCGC
GCGTGACCCC GCTCGGGACA GGAGCCGGAC TCCTGTGCAG CTTCCCTCGG
CCGCCGGGGG CCTCCCCGCG CCTCGCCGGC CTCCAGGCCC CTCCTGGCTG
GCGAGCGGGC GCCACATCTG GCCCGCACAT CTGCGCTGCC GGCCCGGGCG
GGGTCCGGAG AGGGCGCGGC GCGGAGGCAG CCAGGGGTCC GGAAGGCGC
CGTCCGTGCG CTGGGGGCTC GGTCTATGAC GAGCAGCGGG GTCTGCCATG
GGTCGGGGGC TGCTCAGGGC CTGTGGCCGC TGCACATCGT CCTGTGGACG
CGTATCGCCA GCACGATCCC ACCGCACGTT CAGAAGTCGG TTAATAACGA
CATGATAGTC ACTGACAACA ACGGTGCAGT CAAGTTTCCA CAACTGTGTA
AATTTTGTGA TGTGAGATTT TCCACCTGTG ACAACCAGAA ATCCTGCATG
AGCAACTGCA GCATCACCTC CATCTGTGAG AAGCCACAGG AAGTCTGTGT
GGCTGTATGG AGAAAGAATG ACGAGAACAT AACACTAGAG ACAGTTTGCC
ATGACCCCAA GCTCCCCTAC CATGACTTTA TTCTGGAAGA TGCTGCTTCT
CCAAAGTGCA TTATGAAGGA AAAAAAAG CCTGGTGAGA CTTTCTTCAT
GTGTTCTGTG AGCTCTGATG AGTGCAATGA CAACATCATC TTCTCAGAAG
AATATAACAC CAGCAATCCT GACTTGTTGC TAGTCATATT TCAAGTGACA
GGCATCAGCC TCCTGCCACC ACTGGGAGTT GCCATATCTG TCATCATCAT
CTTCTACTGC TACCGCGTTA ACCGGCAGCA GAAGCTGAGT TCAACCTGGG
AAACCGGCAA GACGCGGAAG CTCATGGAGT TCAGCGAGCA CTGTGCCATC
ATCCTGGAAG ATGACCGCTC TGACATCAGC TCCACGTGTG CCAACAACAT
CAACCACAAC ACAGAGCTGC TGCCCATTGA GCTGGACACC CTGGTGGGGA
AAGGTCGCTT TGCTGAGGTC TATAAGGCCA AGCTGAAGCA GAACACTTCA

FIGURE 2A

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GAGCAGTTTG AGACAGTGGC AGTCAAGATC TTTCCCTATG ACCACTATGC
CTCTTGGAAG GACAGGAAGG ACATCTTCTC AGACATCAAT CTGAAGCATG
AGAACATACT CCAGTTCCTG ACGGCTGAGG AGCGGAAGAC GGAGTTGGGG
AAACAATACT GGCTGATCAC CGCCTTCCAC GCCAAGGGCA ACCTACAGGA
GTACCTGACG CGGCATGTCA TCAGCTGGGA GGACCTGCGC AACGTGGGCA
GCTCCCTCGC CCGGGGATTG TCTCACCTCC ACAGTGATCA CACTCCATGT
GGGAGGCCCA AGATGCCCCAT CGTGACACAGG GACCTCAAGA GCTCCAATAT
CCTCGTGAAG AACGACCTAA CCTGCTGCCT GTGTGACTTT GGGCTTTCCC
TGCCTCTTGG ACCCTACTCT TCTGTGGATG ACCTGGCTAA CAGTGGGCAG
GTGGGAAGTG CAAGATACAT GGCTCCAGAA GTCCTAGAAT CCAGGATGAA
TTTGAGAAT GCTGAGTCCT TCAAGCAGAC CGATGTCTAC TCCATGGCTC
TGGTGCTCTG GGAAATGACA TCTCGCTGTA ATGCAGTGGG AGAAGTAAAA
GATTATGAGC CTCCATTTGG TTCCAAGGTG CGGGACCCTG TGGTCGAAAG
CATGAAGGAC AACGTGTTGA GAGATCGAGG CACCAGAAAT TCCAGCTTCT
GGCTCAACCA CCAGGGCATC CAGATGGTGT GTGAGACGTT GACTGAGTGC
TGGGACCACG ACCCAGAGGC CCGTCTCACA GCCCAGTGTG TGGCAGAACG
CTTCAGTGAG CTGGAGCATC TGGACAGGCT CTCGGGGAGG AGCTGCTCGG
AGGAGAAGAT TCCTGAAGAC GGCTCCCTAA AACTACCAA ATAGCTCTTA
TGGGGCAGGC TGGGCATGTC CAAAGAGGCT GCCCCTCTCA CCAAA

FIGURE 2B

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>F1;3FFPEP

Meld of: 3FF6-9 3FF13

MTSSGVCHGS GAAQGLWPLH IVLWTRIAST IPPHVQKSVN NDMIVTDNNG
AVKFPQLCKF CDVRFSTCDN QKSCMSNCSI TSICEKPQEV CVAVWRKNDE
NITLETVCHD PKLPYHDFIL EDAASPKCIM KEKKKPGETF FMCSCSSDEC
NDNIIIFSEY NTSNPDLLLV IFQVTGISLL PPLGVAISVI IIFYCYRVNR
QQKLSSTWET GKTRKLMEFS EHCAIILED RSDISSTCAN NINHNTLELP
IELDTLVGKG RFAEVYKAKL KQNTSEQFET VAVKIFPYDH YASWKDRKDI
ESDINLKHEN ILQFLTAEER KTEL GKQYWL ITAFHAKGNL QEYLTRHVIS
WEDLRNVGSS LARGLSHLHS DHTPCGRPKM PIVHRDLKSS NILVKNDLTC
CLCDFGLSLR LGPYSSVDDL ANSGQVG TAR YMAPEVLES MNLENAESFK
QTDVYSMALV LWEMTSRCNA VGEVKDYEP FGSKVRDPVV ESMKDNVLRD
RGTRNSSFWL NHQGIQMVCE TLTECWDHDP EARLTAQCVA ERFSELEHLD
RLSGRSCSEE KIPEDGSLNT TK*

FIGURE 3